

Intraspecific variation influences community network structure: Tracing the roots of interactions to genetics.

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1.	Main Question: Does selection produce ecological network nestedness? Or, is nestedness primarily a statistical artifact (i.e. more abundance species will be more connected and typically there is an asymptotic shape of ordered species abundance)?	
2.	How does this analysis parallel more common analyses of diversity?	
3.	Read the Geum papers	
4.	Other things to try:	

- (a) Can we look at the inter-connectedness of cushions based on significantly similar? or different communities?

0.1 Questions

- Do the most numerically abundant species have the most connections?
- What traits would increase or decrease the diversity of beneficiary species (i.e. facilitation connections)?

1 Individual level facilitation network models

1.1 Dependent Functions

gdata: read.xls support for 'XLS' (Excel 97-2004) files ENABLED.

gdata: read.xls support for 'XLSX' (Excel 2007+) files ENABLED.

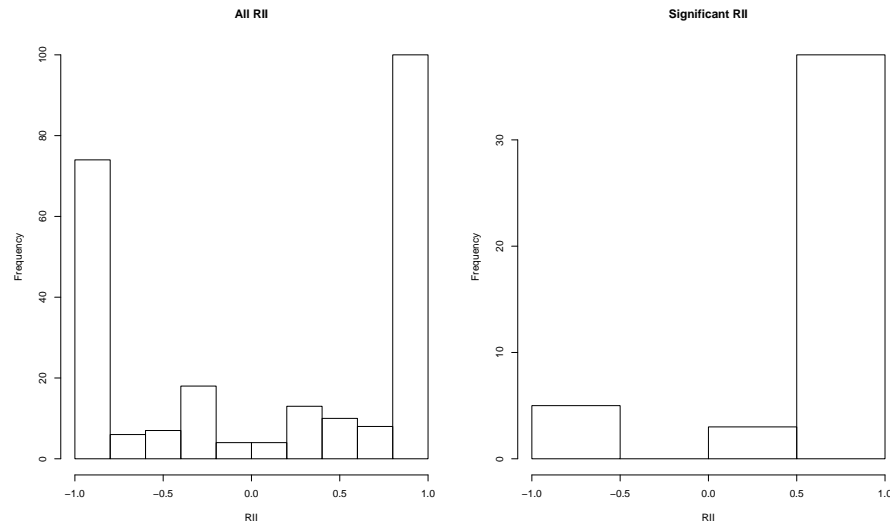
This is bipartite 1.14.
For latest additions type: ?bipartite.
For citation please type: citation("bipartite").
Have a nice time plotting and analysing two-mode networks.

Tools for Social Network Analysis
Version 2.2-0 created on 2010-11-21.
copyright (c) 2005, Carter T. Butts, University of California-Irvine
Type help(package="sna") to get started.

1.2 Generate Network Models

No Test for Significance

1.3 Figures



Checkerboard Units : 4454
C-score (species mean): 23.44211

Checkerboard Units : 297
C-score (species mean): 1.563158

oecosimu with 1000 simulations
simulation method quasiswap
alternative hypothesis: true mean is less than the statistic

Checkerboard Units : 4454
C-score (species mean): 23.44211

	statistic	z	0%	50%	95%	Pr(sim.)
statistic	4454.00000	0.58601	4172.00000	4397.00000	4556	0.2567

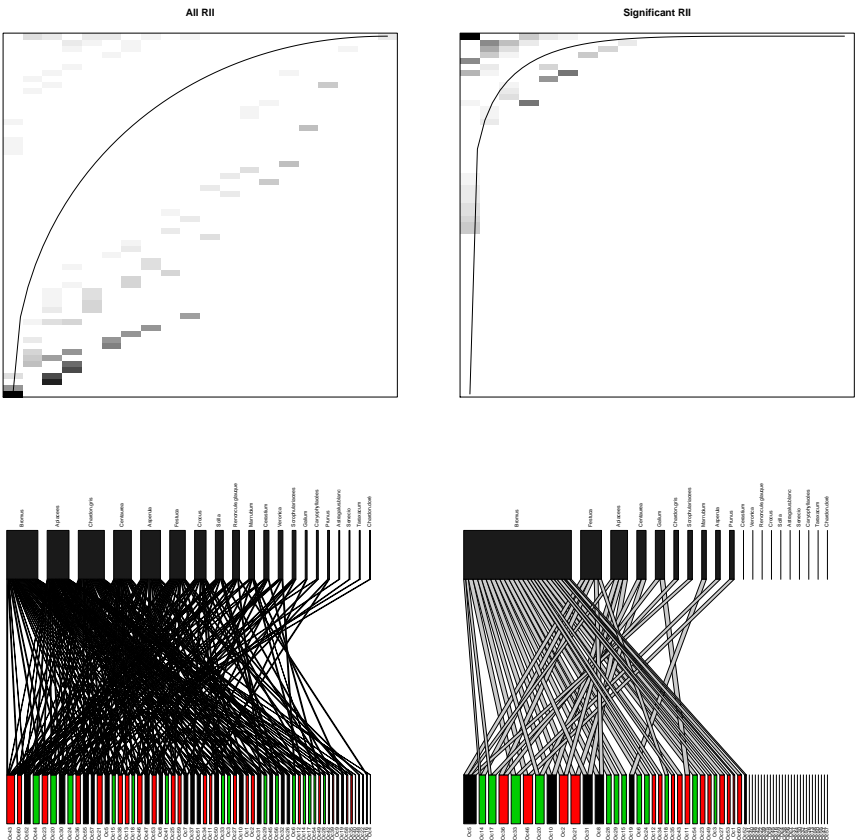
oecosimu with 1000 simulations
simulation method quasiswap

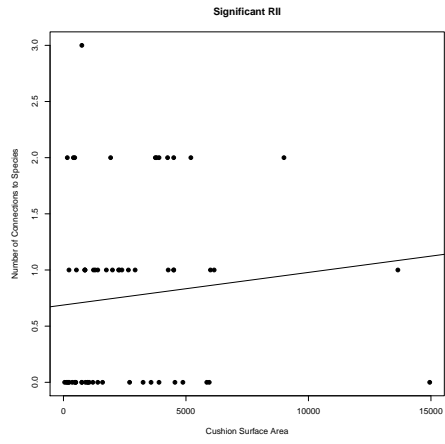
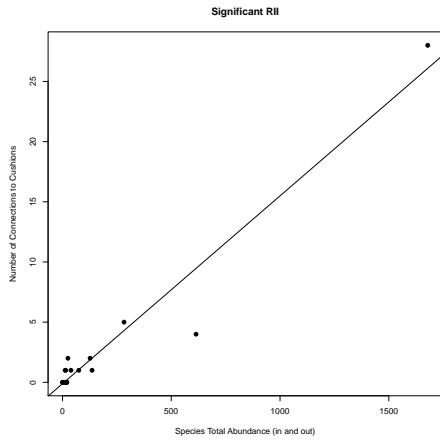
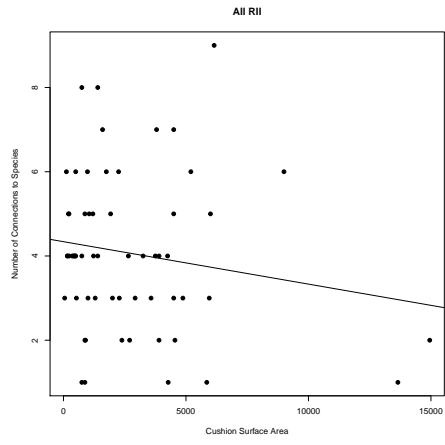
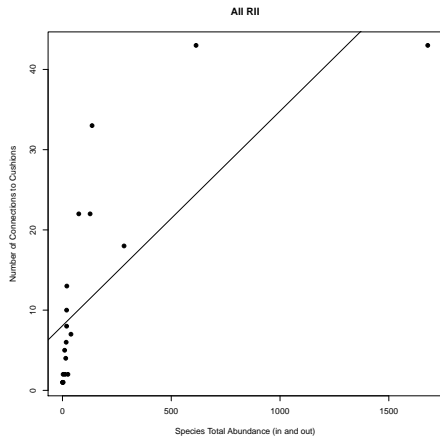
alternative hypothesis: true mean is less than the statistic

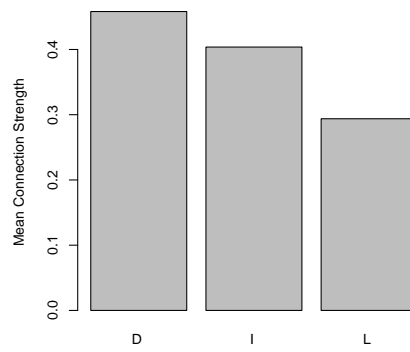
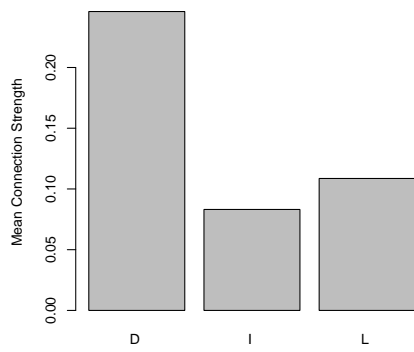
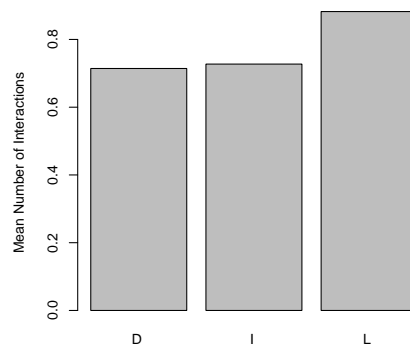
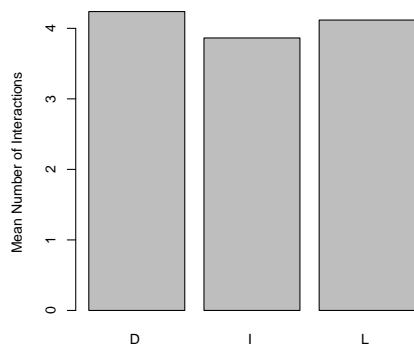
Checkerboard Units : 4454
C-score (species mean): 23.44211

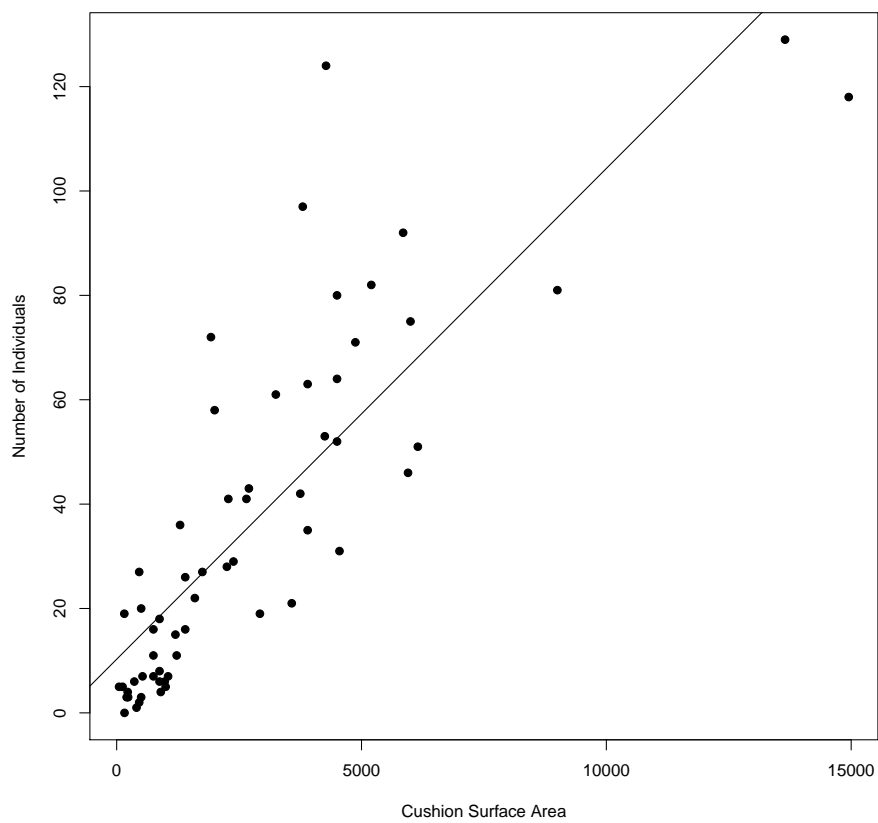
	statistic	z	0%	50%	95%	Pr(sim.)
statistic	4454.00000	0.53066	4192.00000	4400.00000	4566	0.2897

[,1] [,2]
[1,] "D" "RED"
[2,] "I" "BLACK"
[3,] "L" "GREEN"

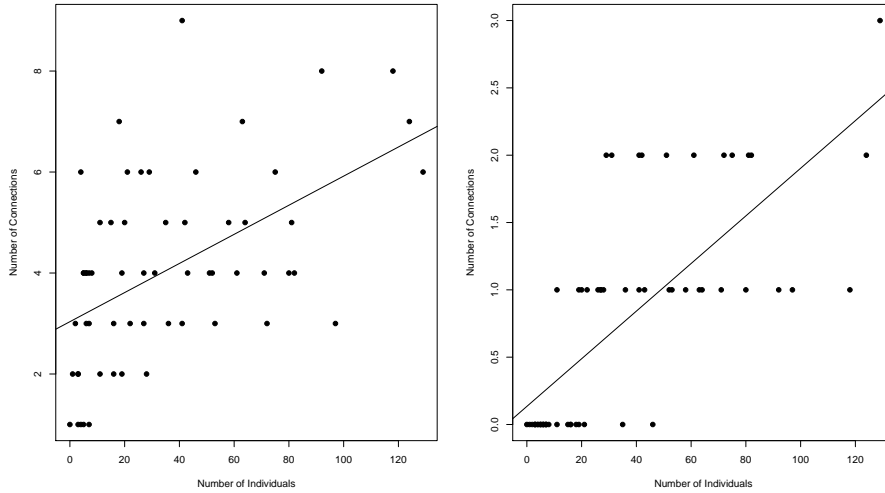








[1] TRUE



	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.0359	0.3040	9.99	0.0000
Oc.ind	0.0288	0.0062	4.63	0.0000

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.1344	0.1059	1.27	0.2095
Oc.ind	0.0177	0.0022	8.15	0.0000

2 Facilitation vs Exclusion

Bromus seems to be the most highly facilitated species, although this could be because it's the most numerically abundant.

```
> Oc.fac <- apply(Oc.order, 2, function(x) length(x[x > 0]))
> Oc.exc <- apply(Oc.order, 2, function(x) length(x[x < 0]))
> barplot(rbind(Oc.fac, Oc.exc), beside = TRUE, las = 2)
> Oc.fac
```

Bromus	Apiacees	Chardon.gris	Centaurea
37	13	13	10

Asperula	Festuca	Crocus	Scilla
4	15	6	4
Renoncule.glaucue	Marrubium	Cerastium	Veronica
7	7	5	5
Scrophulariacees	Galium	CaryophyllacÃl'es	Prunus
4	2	1	1
Astragalus.blanc	Senecio	Taraxacum	Chardon.dorÃl'
0	0	1	0

```

> Oc.fac.. <- apply(Oc.order..., 2, function(x) length(x[x > 0]))
> Oc.exc.. <- apply(Oc.order..., 2, function(x) length(x[x < 0]))
> barplot(rbind(Oc.fac.., Oc.exc..), beside = TRUE, las = 2)
> Oc.fac..

```

Bromus	Festuca	Apiacees	Centaurea
27	5	2	2
Galium	Chardon.gris	Scrophulariacees	Marrubium
2	0	1	1
Asperula	Prunus	Cerastium	Veronica
0	1	0	0
Renoncule.glaucue	Crocus	Scilla	Astragalus.blanc
0	0	0	0
Senecio	CaryophyllacÃl'es	Taraxacum	Chardon.dorÃl'
0	0	0	0

```

> par(mfrow = c(1, 2))
> barplot(rbind(Oc.fac, Oc.exc), beside = TRUE, las = 2)
> barplot(rbind(Oc.fac.., Oc.exc..), beside = TRUE, las = 2)
> Oc.l <- list()
> Oc.l[[1]] <- Oc.com[Oc.env$microsite == "in open", ]
> Oc.l[[2]] <- Oc.com[Oc.env$microsite == "on cushion", ]
> names(Oc.l) <- levels(Oc.env$microsite)
> Oc.net <- list()
> Oc.net[[1]] <- kendall.pairs(Oc.l[[1]], adj.method = "fdr", p.adj = FALSE)
> Oc.net[[2]] <- kendall.pairs(Oc.l[[2]], adj.method = "fdr", p.adj = FALSE)
> names(Oc.net) <- names(Oc.l)
> gplot(abs(Oc.net[[1]]), displaylabels = TRUE, main = "In Open",
+       label.cex = 0.5)
> gplot(abs(Oc.net[[2]]), displaylabels = TRUE, main = "On Cushion",
+       label.cex = 0.5)

```

3 Conduct module detection and then see if there is overlap with the cushion phenotype

[illegible]

4 Examine the monopartite structure and groupings by phenotype

```
> Oc.om <- as.one.mode(Oc.order, project = "lower")
> Oc.om. <- as.one.mode(Oc.order., project = "lower")
```

```

> par(mfrow = c(2, 2))
> gplot(abs(Oc.om), displaylabels = TRUE, gmode = "graph", vertex.col = as.numeric(
> gplot(abs(Oc.om.), displaylabels = TRUE, gmode = "graph", vertex.col = as.numeric(
> legend("topright", legend = sort(unique(Oc.pheno)), pch = 19,
+       col = as.numeric(factor(sort(unique(Oc.pheno))))), box.lwd = 0.5)
> Bs.om <- as.one.mode(Oc.order, project = "higher")
> Bs.om. <- as.one.mode(Oc.order., project = "higher")
> gplot(abs(Bs.om), displaylabels = TRUE, gmode = "graph")
> gplot(abs(Bs.om.), displaylabels = TRUE, gmode = "graph")
> Bs.n <- Bs.om
> Bs.n[Bs.n > 0] <- 0
> Bs.n. <- Bs.om.
> Bs.n.[Bs.n. > 0] <- 0
> par(mfrow = c(2, 2))
> gplot(abs(Bs.om), displaylabels = TRUE, gmode = "graph")
> gplot(abs(Bs.om.), displaylabels = TRUE, gmode = "graph")
> gplot(abs(Bs.n), displaylabels = TRUE, gmode = "graph")
> gplot(abs(Bs.n.), displaylabels = TRUE, gmode = "graph")

```

